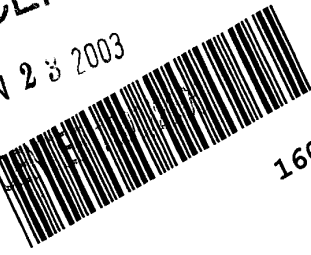


S. Ungar.

RECEIVED

JUN 23 2003

TECH



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/234,290B

Input Set : A:\10274-008003.txt
Output Set : N:\CRF4\06172003\I234290B.raw

4 <110> APPLICANT: Burkly, Linda C.
6 <120> TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES
9 <130> FILE REFERENCE: 10274-008003
11 <140> CURRENT APPLICATION NUMBER: US 09/234,290B
12 <141> CURRENT FILING DATE: 1999-01-20
14 <150> PRIOR APPLICATION NUMBER: US 08/447,118
15 <151> PRIOR FILING DATE: 1993-05-22
17 <150> PRIOR APPLICATION NUMBER: US 08/029,330
18 <151> PRIOR FILING DATE: 1993-02-09
20 <150> PRIOR APPLICATION NUMBER: PCT/US94/01456
21 <151> PRIOR FILING DATE: 1994-02-09
24 <160> NUMBER OF SEQ ID NOS: 19
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 360
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (0)...(0)
36 <223> OTHER INFORMATION: pBAG159 insert: HP1/2 heavy
37 chain variableregion; amino acid 1
38 is Glu (E) but Gln (Q) may be substituted
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)...(360)

ENTERED

W--> 44 <400> 1
45 gtc aaa ctg cag cag tct ggg gca gag ctt gtg aag cca ggg gcc tca 48
46 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser 96
47 1 5 10
49 gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc tat 15
50 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr 30
51 20 25
53 atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att gga 144
54 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly 45
55 35 40
57 agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc cag 192
58 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln 60
59 50 55
61 gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg ctg 240
62 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu 80
63 65 70 75
65 cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt gca 288
66 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala

RAW SEQUENCE LISTING

DATE: 06/17/2003

PATENT APPLICATION: US/09/234,290B

TIME: 15:08:21

Input Set : A:\10274-008003.txt

Output Set: N:\CRF4\06172003\I234290B.raw

```

67          85          90          95
69 gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc caa      336
70 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
71          100          105          110
73 ggg acc acg gtc acc gtc tcc tca      360
74 Gly Thr Thr Val Thr Val Ser Ser
75          115          120
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 120
80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens
83 <400> SEQUENCE: 2
84 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
85 1          5          10          15
86 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
87          20          25          30
88 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
89          35          40          45
90 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
91          50          55          60
92 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
93 65          70          75          80
94 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
95          85          90          95
96 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
97          100          105          110
98 Gly Thr Thr Val Thr Val Ser Ser
99          115          120
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 318
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <220> FEATURE:
107 <221> NAME/KEY: misc_feature
108 <222> LOCATION: (0)...(0)
109 <223> OTHER INFORMATION: pBAG172 insert: HP1/2
110 light chain variable region
113 <221> NAME/KEY: CDS
114 <222> LOCATION: (1)...(318)
115 <223> OTHER INFORMATION: HP1/2 light chain variable region
W--> 118 <400> 3
119 agt att gtg atg acc cag act ccc aaa ttc ctg ctt gtt tca gca gga      48
120 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
121 1          5          10          15
123 gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat      96
124 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
125          20          25          30
127 gta gct tgg tac caa cag aag cca ggg cag tct cct aaa ctg ctg ata      144
128 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

```

RAW SEQUENCE LISTING

DATE: 06/17/2003

PATENT APPLICATION: US/09/234,290B

TIME: 15:08:21

Input Set : A:\10274-008003.txt

Output Set: N:\CRF4\06172003\I234290B.raw

```

129          35          40          45
131 tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc      192
132 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
133          50          55          60
135 agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct      240
136 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
137 65          70          75          80
139 gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac      288
140 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
141          85          90          95
143 acg ttc gga ggg ggg acc aag ctg gag atc      318
144 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
145          100          105
148 <210> SEQ ID NO: 4
149 <211> LENGTH: 106
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 4
154 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
155 1          5          10          15
156 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
157          20          25          30
158 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
159          35          40          45
160 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
161          50          55          60
162 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
163 65          70          75          80
164 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
165          85          90          95
166 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
167          100          105
169 <210> SEQ ID NO: 5
170 <211> LENGTH: 429
171 <212> TYPE: DNA
172 <213> ORGANISM: Homo sapiens
174 <220> FEATURE:
175 <221> NAME/KEY: CDS
176 <222> LOCATION: (1)...(429)
178 <221> NAME/KEY: sig_peptide
179 <222> LOCATION: (1)...(57)
W--> 181 <221> mat_peptide
182 <222> LOCATION: (58)...(429)
W--> 184 <221> misc_feature
185 <222> LOCATION: (0)...(0)
186 <223> OTHER INFORMATION: pBAG195 insert: AS heavy chain variable region
W--> 189 <400> 5
190 atg gac tgg acc tgg agg gtc ttc tgc ttg ctg gct gta gca cca ggt      48
191 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly

```

RAW SEQUENCE LISTING

DATE: 06/17/2003

PATENT APPLICATION: US/09/234,290B

TIME: 15:08:21

Input Set : A:\10274-008003.txt

Output Set: N:\CRF4\06172003\I234290B.raw

```

192          -15          -10          -5
194 gcc cac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga      96
195 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
196          1          5          10
198 cct agc cag acc ctg agc ctg acc tgc acc gcg tct ggc ttc aac att      144
199 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
200          15          20          25
202 aaa gac acc tat atg cac tgg gtg aga cag cca cct gga cga ggt ctt      192
203 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
204          30          35          40          45
206 gag tgg att gga agg att gat cct gcg agt ggc gat act aaa tat gac      240
207 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
208          50          55          60
210 ccg aag ttc cag gtc aga gtg aca atg ctg gta gac acc agc agc aac      288
211 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
212          65          70          75
214 cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtc      336
215 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
216          80          85          90
218 tat tat tgt gca gac gga atg tgg gta tca acg gga tat gct ctg gac      384
219 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
220          95          100          105
222 ttc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gag tcc      429
223 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
224 110          115          120
227 <210> SEQ ID NO: 6
228 <211> LENGTH: 143
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <220> FEATURE:
233 <221> NAME/KEY: SIGNAL
234 <222> LOCATION: (1)...(19)
236 <400> SEQUENCE: 6
237 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
238          -15          -10          -5
239 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
240          1          5          10
241 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
242          15          20          25
243 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
244          30          35          40          45
245 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
246          50          55          60
247 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
248          65          70          75
249 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
250          80          85          90
251 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
252          95          100          105

```

RAW SEQUENCE LISTING

DATE: 06/17/2003

PATENT APPLICATION: US/09/234,290B

TIME: 15:08:22

Input Set : A:\10274-008003.txt

Output Set: N:\CRF4\06172003\I234290B.raw

```

253 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
254 110                      115                      120
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 384
258 <212> TYPE: DNA
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <221> NAME/KEY: CDS
263 <222> LOCATION: (1)...(384)
265 <221> NAME/KEY: sig_peptide
266 <222> LOCATION: (1)...(57)
W--> 268 <221> mat_peptide
269 <222> LOCATION: (58)...(384)
W--> 271 <221> misc_feature
272 <222> LOCATION: (0)...(0)
273 <223> OTHER INFORMATION: pBAG198 insert: VK (SVMDY) light chain variable
274      region
W--> 277 <400> 7
278 atg ggt tgg tcc tgc atc atc ctg ttc ctg gtt gct acc gct acc ggt      48
279 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
280      -15                      -10                      -5
282 gtc cac tcc agc atc gtg atg acc cag agc cca agc agc ctg agc gcc      96
283 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
284      1                      5                      10
286 agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag agt gtg      144
287 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
288      15                      20                      25
290 act aat gat gta gct tgg tac cag cag aag cca ggt aag gct cca aag      192
291 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
292 30                      35                      40                      45
294 ctg ctg atc tac tat gca tcc aat cgc tac act ggt gtg cca gat aga      240
295 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
296      50                      55                      60
298 ttc agc ggt agc ggt tat ggt acc gac ttc acc ttc acc atc agc agc      288
299 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
300      65                      70                      75
302 ctc cag cca gag gac atc gcc acc tac tac tgc cag cag gat tat agc      336
303 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
304      80                      85                      90
306 tct ccg tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt aag      384
307 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
308      95                      100                      105
311 <210> SEQ ID NO: 8
312 <211> LENGTH: 128
313 <212> TYPE: PRT
314 <213> ORGANISM: Homo sapiens
316 <220> FEATURE:
317 <221> NAME/KEY: SIGNAL
318 <222> LOCATION: (1)...(19)

```

VERIFICATION SUMMARY

DATE: 06/17/2003

PATENT APPLICATION: US/09/234,290B

TIME: 15:08:23

Input Set : A:\10274-008003.txt

Output Set: N:\CRF4\06172003\I234290B.raw

L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:118 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:189 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:268 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:271 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:277 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:363 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:369 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:372 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:378 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:381 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9